**Fig. 1**

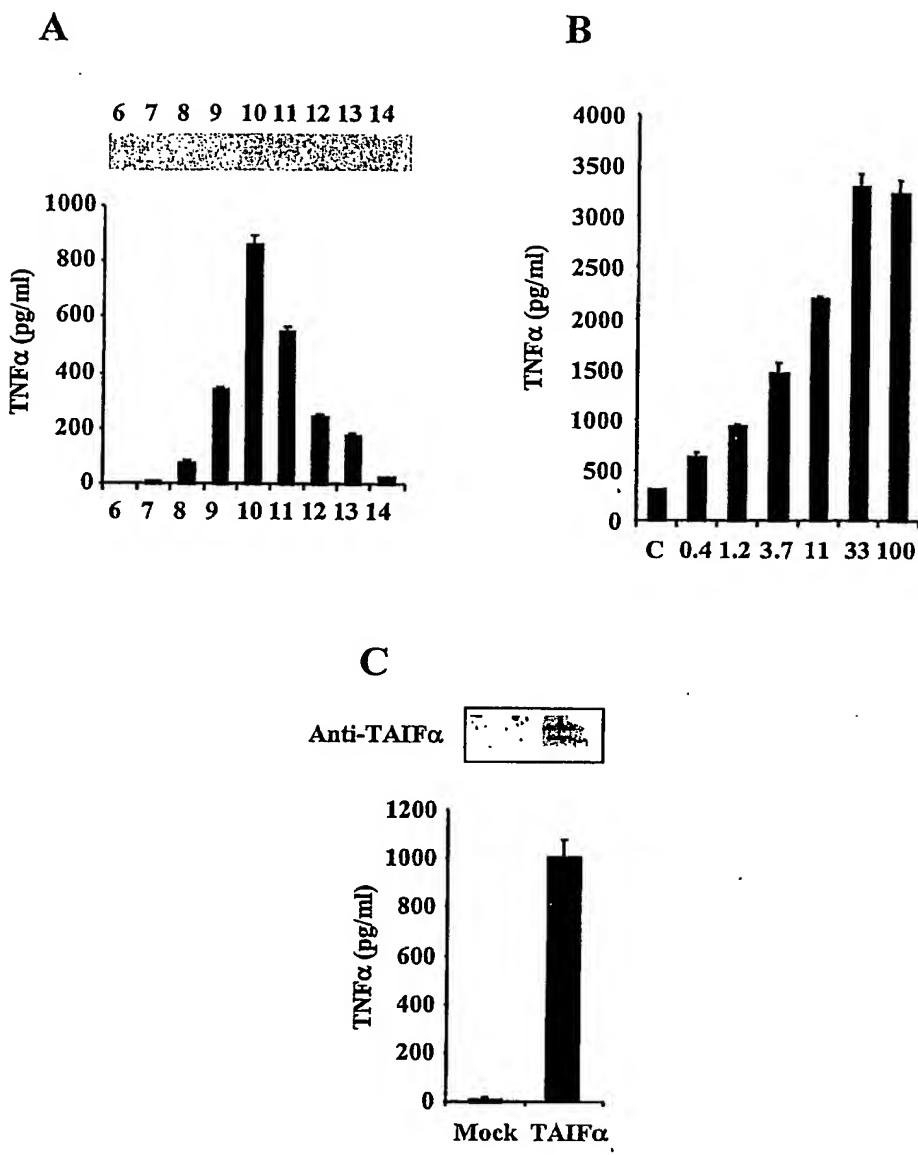


Fig. 2

IL-32 α	ATGTGCTTCCCGAAGGCCTCTCTGATGACATGAAGAAGCTGAAGGCCGAATG-----
IL-32 β	ATGTGCTTCCCGAAGGCCTCTCTGATGACATGAAGAAGCTGAAGGCCGAATG-----
IL-32 γ	ATGTGCTTCCCGAAGGCCTCTCTGATGACATGAAGAAGCTGAAGGCCGAATGGTAATG
IL-32 δ	-----ATGAAGAAGCTGAAGGCCGAATG-----
IL-32 α	-----
IL-32 β	-----
IL-32 γ	CTCCTCCCTACTTCTGCTCAGGGTTGGGGCCTGGGTCTCAGCGTGTGACACTGAGGAC
IL-32 δ	-----
IL-32 α	-----
IL-32 β	-----
IL-32 γ	ACTGTGGGACACCTGGACCCTGGAGGGACAAGGATCCGGCCCTTGGTGCCAACCTGC
IL-32 δ	-----
IL-32 α	-----CACCAAGGCTATAGAAAGATTTATGATAAAATGC AAAATGCAGAATCA
IL-32 β	-----CACCAAGGCCATAGAAAGATTTATGATAAAATGC AAAATGCAGAATCA
IL-32 γ	CTCTCTTCACAGCACCAAGGCCATAGAAAGATTTATGATAAAATGC AAAATGCAGAATCA
IL-32 δ	-----CACCAAGGCCATAGAAAGATTTATGATAAAATGC AAAATGCAGAATCA
IL-32 α	GGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32 β	GGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32 γ	GGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32 δ	GGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTGGAGGACGACTTCAAAGAGGGCTAC
IL-32 α	CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32 β	CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32 γ	CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA
IL-32 δ	CTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCCTCTACTTGAA

Fig. 3A

IL-32 α	AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCGATGTTGAGGAT
IL-32 β	AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCGATGTTGAGGAT
IL-32 γ	AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCGATGTTGAGGAT
IL-32 δ	AAAGAAAGAGATGGATTACGGTGCCGAGGCAACAGATCCCGATGTTGAGGAT
IL-32 α	CCCGCAACCAGGGAGCCTGGGGAGAGCTTTGTGACAAGGT-----
IL-32 β	CCCGCAACCAGGGAGCCTGGGGAGAGCTTTGTGACAAGGT-----CATGAGATGGTTCCAGGCC
IL-32 γ	CCCGCAACCAGGGAGCCTGGGGAGAGCTTTGTGACAAGGT-----CATGAGATGGTTCCAGGCC
IL-32 δ	CCCGCAACCAGGGAGCCTGGGGAGAGCTTTGTGACAAGGT-----CATGAGATGGTTCCAGGCC
IL-32 α	-----
IL-32 β	ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGTTCTGGCCTGGTGAAGGAGAAGGTG
IL-32 γ	ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGTTCTGGCCTGGTGAAGGAGAAGGTG
IL-32 δ	ATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGTTCTGGCCTGGTGAAGGAGAAGGTG
IL-32 α	-----
IL-32 β	GTGGCCCTGGTCCATGCAGTCAGGCCTCTGGAAACAGTTCCAGAGTTCTGCTGCTCT
IL-32 γ	GTGGCCCTGGTCCATGCAGTCAGGCCTCTGGAAACAGTTCCAGAGTTCTGCTGCTCT
IL-32 δ	GTGGCCCTGGTCCATGCAGTCAGGCCTCTGGAAACAGTTCCAGAGTTCTGCTGCTCT
IL-32 α	-----TCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32 β	CTGTCAGAGCTTTCATGTCCTCTTCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32 γ	CTGTCAGAGCTTTCATGTCCTCTTCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32 δ	CTGTCAGAGCTTTCATGTCCTCTTCAGTCCTACGGAGCCCCACGGGGGGACAAGGAG
IL-32 α	GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGA
IL-32 β	GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGA
IL-32 γ	GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGA
IL-32 δ	GAGCTGACACCCCAGAAGTGCTCTGAACCCCAATCCTCAAAATGA

Fig. 3B

A

	1	Myr
IL-32 α	MCFPKVLSDDMKKLKARM-----	
IL-32 β	MCFPKVLSDDMKKLKARM-----	
IL-32 γ	MCFPKVLSDDMKKLKARMVMLLPTSAQGLGAWVSACDTEDTVGHGPWRDKDPALWCQLC	
IL-32 δ	-----MKKLKARM-----	
	61	Myr
IL-32 α	----HQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAAYYEEQHPELTPILLE	
IL-32 β	----HQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAAYYEEQHPELTPILLE	
IL-32 γ	LSSQHQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAAYYEEQHPELTPILLE	
IL-32 δ	----HQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAAYYEEQHPELTPILLE	
	121	Gly
IL-32 α	KERDGLRCRGNRSPVPDVDPATEEPGESFCDK-----	
IL-32 β	KERDGLRCRGNRSPVPDVDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAWVKEKV	
IL-32 γ	KERDGLRCRGNRSPVPDVDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAWVKEKV	
IL-32 δ	KERDGLRCRGNRSPVPDVDPATEEPGESFCDKVMRWFQAMLQRLQTWWHGVLAWVKEKV	
	181	Myr
IL-32 α	-----SYGAPRGDKEELTPQKCSEPOQSSK	
IL-32 β	VALVHAVQALWKQFQSFCCSLSLFMSSFQS-----SYGAPRGDKEELTPQKCSEPOQSSK	
IL-32 γ	VALVHAVQALWKQFQSFCCSLSLFMSSFQS-----SYGAPRGDKEELTPQKCSEPOQSSK	
IL-32 δ	VALVHAVQALWKQFQSFCCSLSLFMSSFQS-----SYGAPRGDKEELTPQKCSEPOQSSK	

B

	1	
huIL-32 β	MCFPKVLSDDMKKLKARMHQAIERFYDKMQNAESGRGQVMSSLAELEDDFKEGYLETVAA	
EqIL-32	MGYPKTSREDNERWKIRFHSTLDRWLDDIEVQSQGEQVDSLGEDLEEKFSENILDAVEE	
BoIL-32	MCFAKGVPYDQASLRSIMHKRVDDFCDFKMGNPE-EAQMEAALDETEEGLSEDICEFIED	
Consensus	*-----*-----*-----*-----*-----*	
	61	
huIL-32 β	YYEEQHPELTPPLEKERDGLRCRGNRSPV----PDVEDP---ATE--EPGESFCDFKVMR	
EqIL-32	HHQKNNSESAPLLPDVKPRLRRRAQKSSVLPNEPEGPGILQVEALEAPEPEESFWVRAWR	
BoIL-32	HIQENLPES--LQESSPL-LQEARGVRRRIQRPSV---SARLEVQNPEESI---WA	
Consensus	-----*-----*-----*-----*-----*-----*-----*-----*	
	121	
huIL-32 β	WFQAMLQR-L-QTWWHGVLAWVKEKVV-----LVHAVQALWKQFQS---FCCSLSELF	
EqIL-32	SFMGMLQR-LKQRWQAVLA-WVREKVAAGWQA--LCSVAQSIINSVLES---FCSYMAGLF	
BoIL-32	RALGRFQVIL-QSLQQRC--WDALTWLREKAVTFLEAICSVVKAVLGVLTDFCSSVGOLF	
Consensus	-----*-----*-----*-----*-----*-----*-----*-----*	
	181	
huIL-32 β	MSSF---QSYGAPRGDKEELTPQKCSEPOQSSK	
EqIL-32	RYH---IQV-----	
BoIL-32	---GNLIQV-----	
Consensus	-----*-----	

Fig. 4

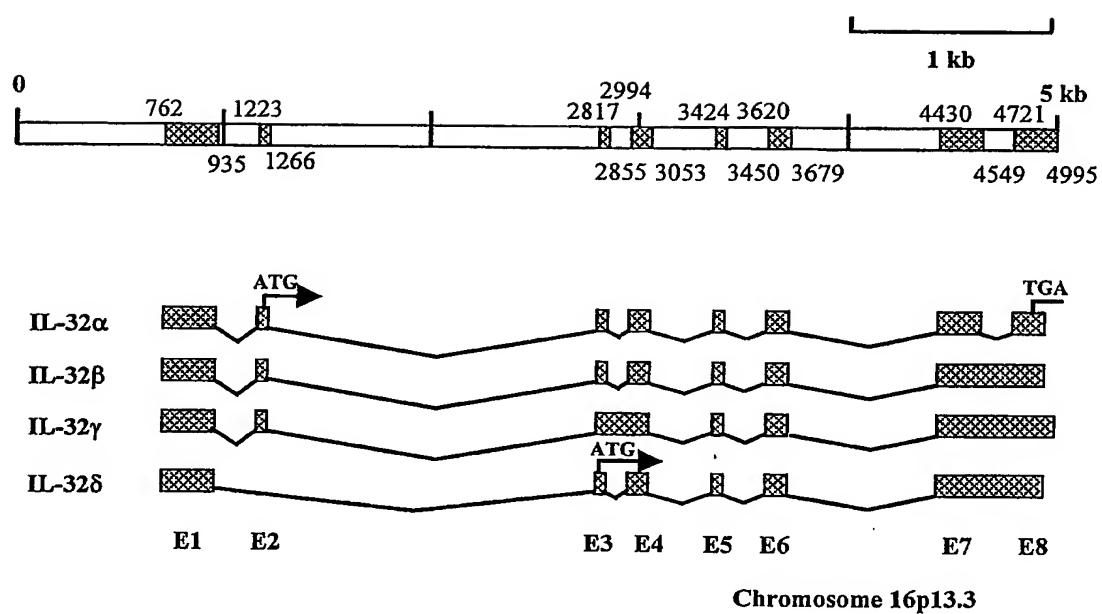


Fig. 5

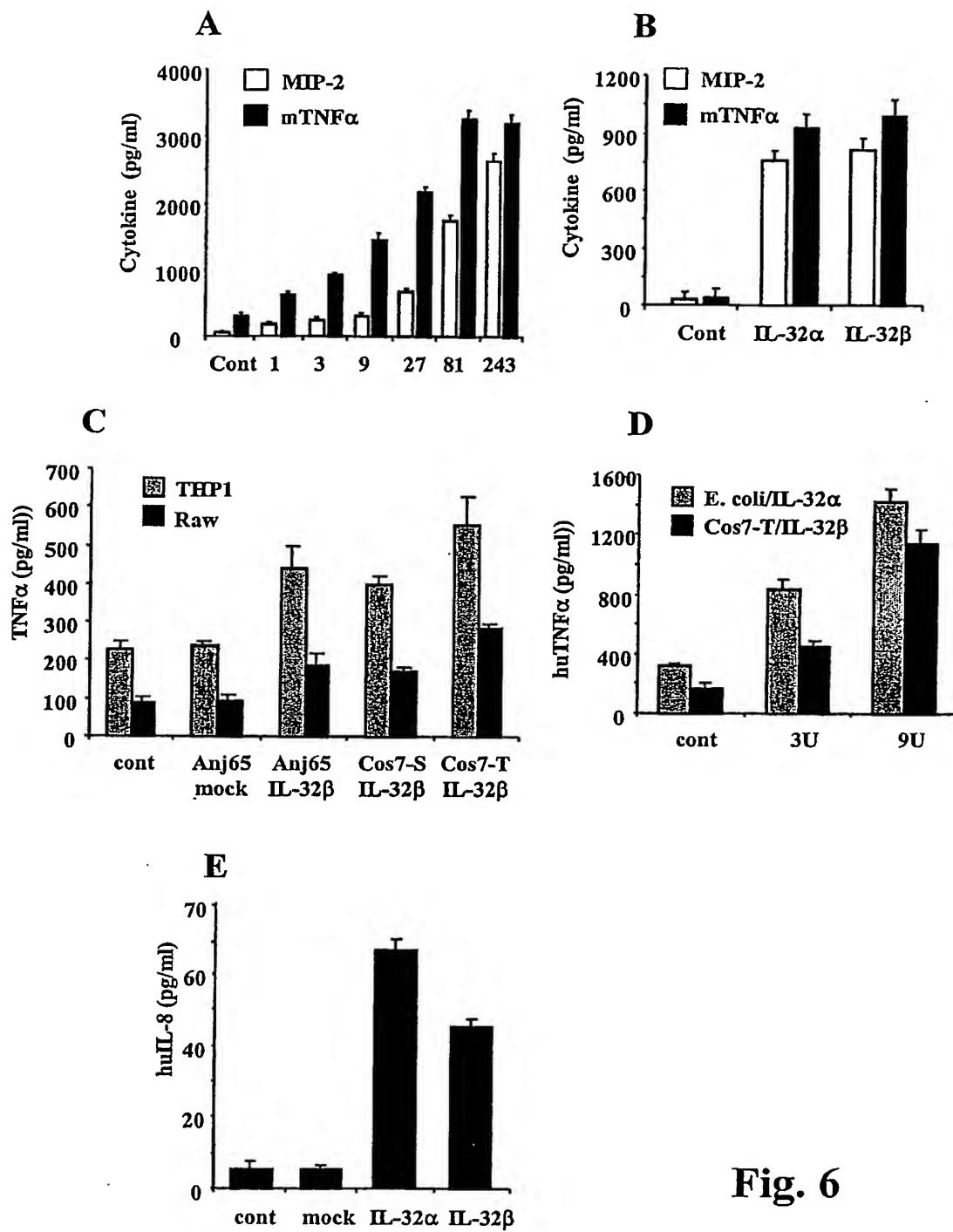


Fig. 6

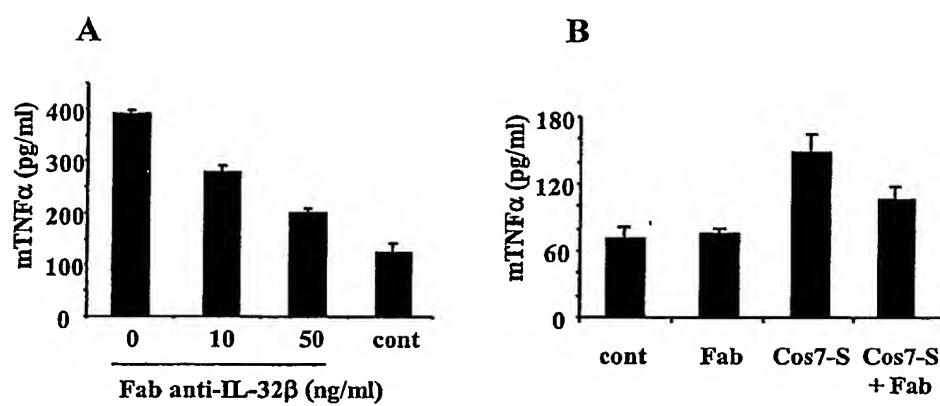


Fig. 7

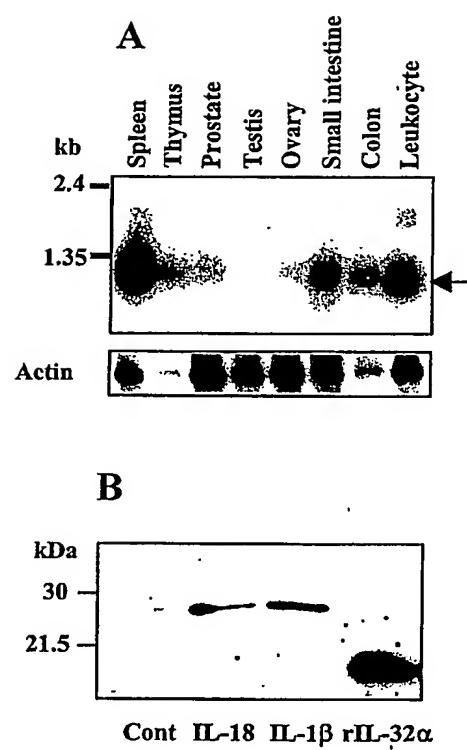
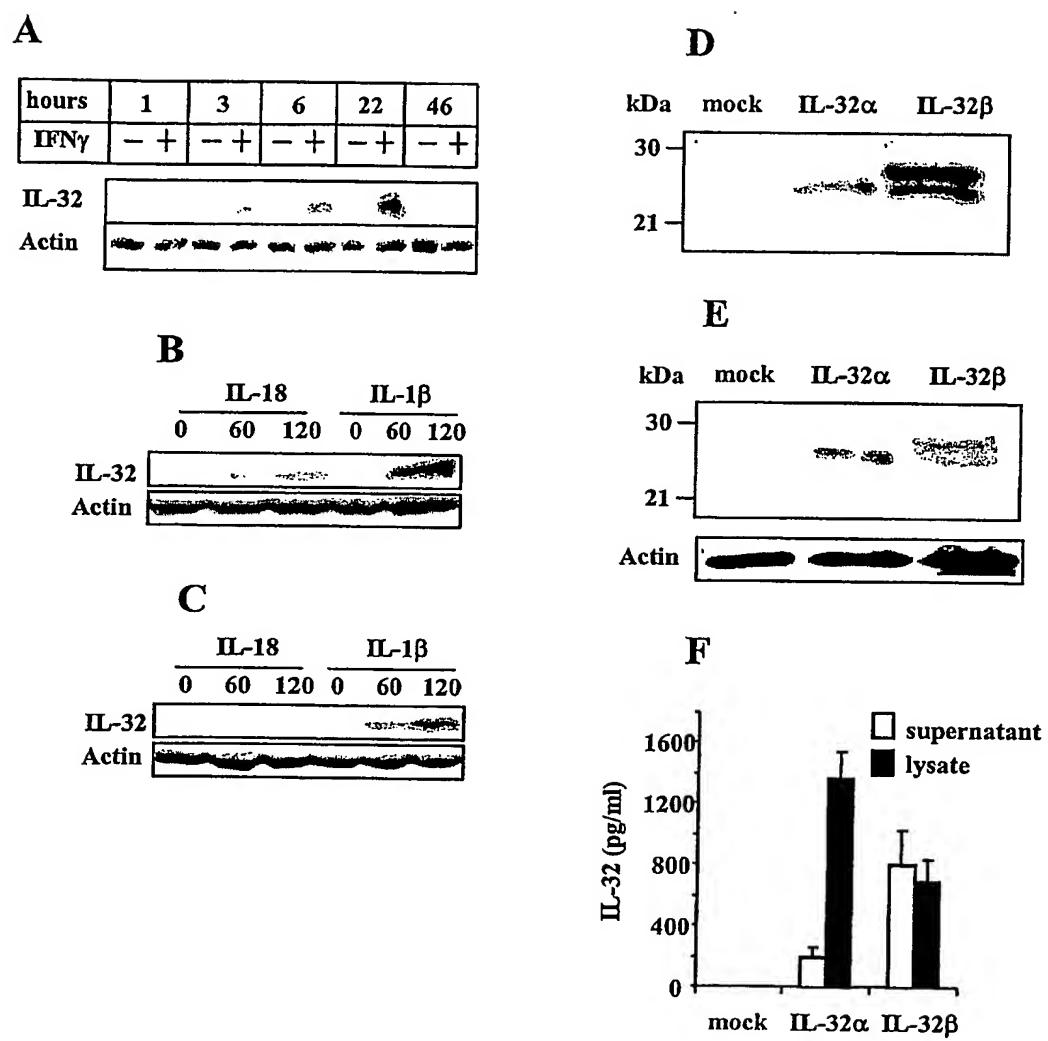
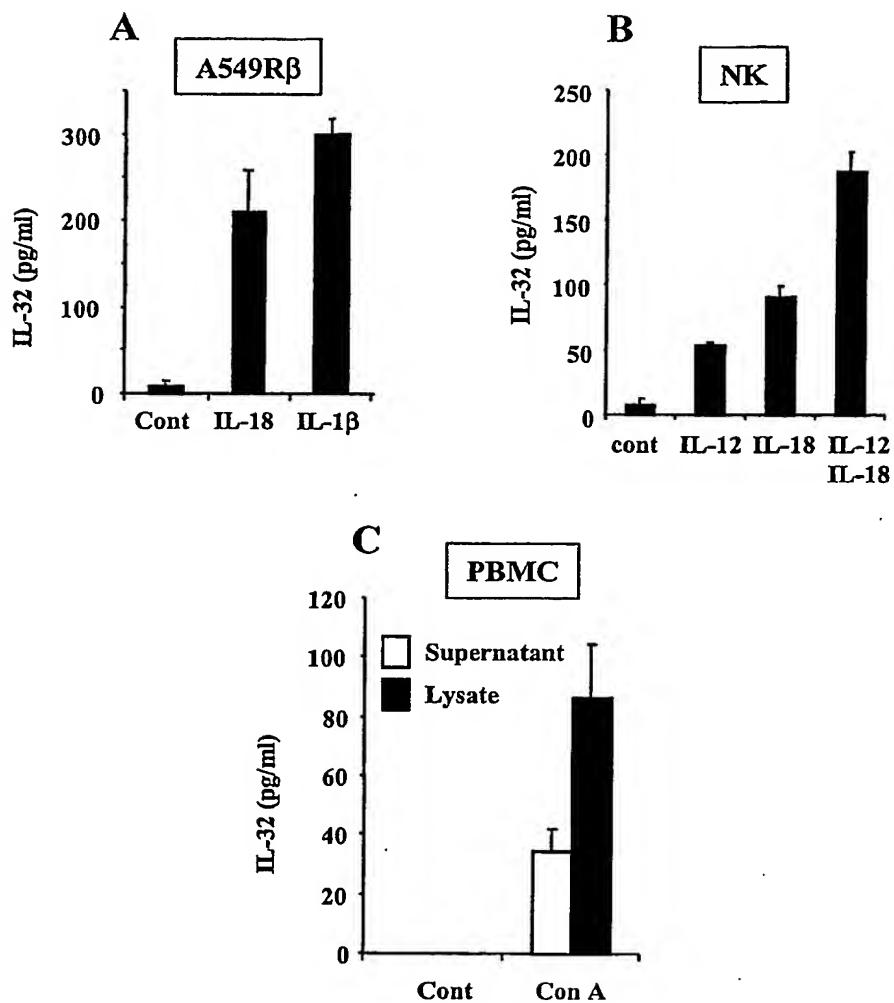


Fig. 8

**Fig. 9**

**Fig. 10**

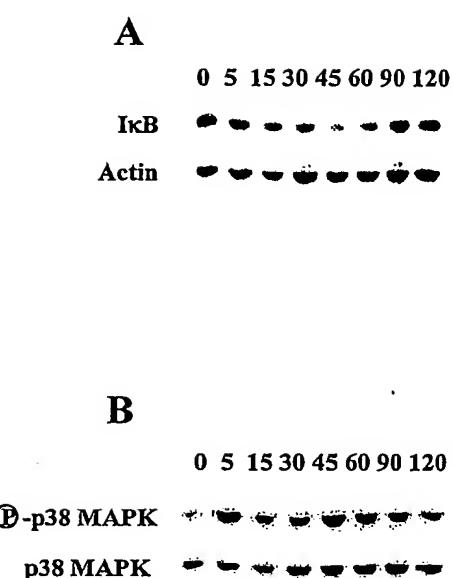


Fig. 11

A

EqIL-32 alpha (SEQ ID NO:18)

MGYPKTSREDNERWKIRFHSTLDRWLDIIEVQSQGEEQVCQCAPTPCSRNLGRRVVTMTMRRKNVPPQVD
LGPLTSPFSORTFRSDLCHLPTLDLSSLTSLLCTAWPPCPCSGFLLOQV

B

EqIL-32 alpha (SEQ ID NO:19)

GCACGAGCTCGGCCGTGTGCTGAGAGGCCCTGGGCAGGCACAGCCCTGGAATCCTGAGCTGCCATG
GGCTACCCAAGACGTCCAGAGAACATGAACTGGAAAGATCCGATTTCACAGCACTTAGACC GGTT
GGCTTGATGATATCGAAGTCAATCCAAGGAGAGGAACAGGTGTGTCAGTGTGCTCCCACGCCCTGCTC
CCGTAACCTCGGGGGTGGTGTACGATGACGATGAGGAGGAAGAACGTGCCACCTCAGGTCGATT TA
GGCCCTTTGACGTCCCCCTTTCACAGAGAACCTTCAGAAGT GACCTT GCCACCTGCCTACCCTTGACC
TGTCTTGACCACCTCCCTCACCTCCTGCTGTGACAGCCTGGCCACCCCTGCCACCATGCACTT CCGT
CTCAGGTTCTCTGCAGGTCTGACTTGTGGCTCCAGGCATATGTCTTAATAAGTTGTG

C

EqIL-32 beta (SEQ ID NO:16)

MGYPKTSREDNERWKIRFHSTLDRWLDIIEVQSQGEQVDLGLLEDLEEKFSENILD
DAVEHHQKNNSA
PLLPDVKPRLLRRAQKSSVLPNEPEGPGILQVEALEAPEPEESFWVRAWSFMGMLQR
LKQRWQAVLAWV
REKVAAGWQALCSVAQSINSVLESFCSYMAGLFRYHIQV

D

EqIL-32 beta (SEQ ID NO:20)

CTGAGAGGCCCTGGGCAGGCACAGCCCTGGAATCCTGAGCTGCCATGGCTACCCCAAGACGTCCAG
AGAAGACAATGAACTTGGAAAGATCGATTTCACAGCACTTAGACCGGTGGCTTGATGATATCGAAGTT
CAATCCAAGGAGAGGAACAGGTCATTAGGCCTAGAACCTGGAGGAAAATTCACTGAAAAACATT
TTGACGCCGTGGAGGAGCACCATCAGAAGAACACTCAGAATCTGGCCTTACTTCCTGACGTGAAGCC
CAGGTTACGTCGAGAGCTCAGAAGTCTCTGCTCTAACCTGAAACCTGAGGGTCCAGGGATCTGCAA
GTTGAGGCTCTAGAGGCACCCGAGCCTGAAGAAAGCTTTGGGTCAAGACATGGAGGTGTTATGGGGA
TGCTACAGCGACTGAAGCAGAGGTGGCAGGCTGTAUTGGCCTGGGTGCGAGAGAAGGTGGCTGCTGGCTG
GCAGGCCCTATGCACTGTGGCCAGTCCATTAAATAGTGTGCTTGAGAGTTCTGCTCCTATATGGCTGG
TTGTTTAGGTACACATCCAGGTCTAGGGGCCCATGGGTCCAGGAGGGTAGCCACACCTTGAGCC
CTTGACGTCCCCCTTTCACAGAGAACCTCAGAAGTGAACCTTGGCCACCTGCCTACCCCTGACCTGTC
CTTGACCACCTCCCTCACCTCCTGCTGTGCACAGCCTGCCACCCGCCACATGCACCTCCTGCTCA
GGTTCTCTGAGGTCTGACTTGTGGCTCCAGCGCATAGTCTT

Fig. 12

A**BoIL-32 beta (SEQ ID NO:17)**

MCFAKGVPYDQASLRSIMHKRVDDFCDKMGNPEEEAQMEAALDETEEGLSEDICEFIEDHIQENLPESLQ
 ESSPLLQEARQGVRRRIQRPSVSARLEVQNPEESIWARALGRFQVILQSLQQRCWDALTWLREKAVTFLE
 AICSVVKAVLGVLTDFFCSSVGQLFGNLIQV

B**BoIL-32 beta (SEQ ID NO:21)**

CGGATTCCGGGATGCTCAGCTGGAGCTCTGGCTGCAGGATCTCAGGTCCCTCGGGAGGACCTAAGCC
 ACCATGTGCTTCGCTAACGGAGTCCCATAATGACCAGGCTCTGAGGTCCATAATGCACAAACGGGTGG
 ATGATTTCTGTGATAAGATGGAAATGAACCAAGAAGAACAGATGGAGGCAGCCCTAGATGAGACGGA
 GGAGGGACTCAGCAGGACATCTGTGAATTATAGAAGATCACATTCAAGAGAACCTCCGAATCCCTG
 CAGGAGTCCAGTCCTGCTTCAGGAAGCAGGCAAGGAGTACGCCGAGAATCCAGAGAACCTTCAGTCT
 CTGCCGTCTGGAGGTCCAGAACATCCGAAGAGAGCATCTGGCCAGAGCCCTGGGAGGTTCCAAGTAAT
 TCTGCAGAGTCTCCAGCAGCGGTGTTGGGATGCGCTCACCTGGCTGCGGGAGAACGGGTGACCTTCCTG
 GAGGCCATCTGCAGTGTGGAAGGCCGCTTGGGAGTGCTGACGGATTCTGCTCCTCTGTGGGCAGC
 TCTCGGAAACCTCATCAGGTCTAGGAGCCGAGGTGGTCTGGAGGAACCTCCCTCATCTAGGAGGC
 CCTGCACCATCCCCCTCCAGAAACCATCTTGTGAAGCGACCTTGCACTCCTGCTCACCTTGACCCAT
 CCTTTAACGTGCCCTCACCTCCTGT

C**BoIL-32 gamma (SEQ ID NO:22)**

MCFTKRDPRVILASFRVLMVRSSFPRIAGVRAWLLGEAENILAHGPSREKNRDSFTQVHLCSQHNLD
 EFFDTMENEPEGAQMEEAVLAETKEKFIDFKVMDNHIQENSPELKESSPLLQEAEVRCRIQRRSVS
 TSLEVQNPEESIWARALRQFLGILQSFLSGCRDALTWLWEKAACLQAICSAVEALWEVLTDFCSFVGQL
 LCRSLIQV

D**BoIL-32 gamma (SEQ ID NO:23)**

CGGGATCTCAGCTGGAGCTCTGGCTGCAGGATCTCAGGTCCAGGGCAGGACCTAAGCCACCATGTGC
 TTCACTAAGAGAGACCCACGTGTCCTGGCTTCTTCAGGGTGTAAATGGAAGACTCATTCCACGTA
 TAGCTGGGTTCTGGGAGGCCTGGTTCTGCTGGGTGAAGCTGAGAACATTCTGGCCACTGGGACCCAG
 CAGGGAGAAGAACCGAGATTCTTACTCAAGTCCATCTCTGTTACAGCACACACCTGTAGATGAATT
 TTGCATACAATGGAAAATGAACCAGAAGGAGCACAGATGGAGGCAGTCCTAGCAGAGACTAAGGAGAAAT
 TCATCAAGGAGCCCTTAAAGTCATGGATAATCACATTCAAGAGAACAGTCCCAGAACCTGAAGGAGTC
 CAGTCCTTGCTTCAGGAAGCACGCAAGAACAGTACGCTGCAGAACATCCAGAGACGCTCCGTCTCACCTCT
 CTGGAGGTCCAGAACATCCGAAGAGAGCATCTGGCCAGAGCCCTGCCAGTTCTGGCATTCTGCAGA
 GTTTCCTGTCCGGGTGTGGGATGCGCTCACCTGGCTGTTGGAGAACGGCCGGCCTGCCTACAGGCCAT
 CTGCAGTGCGGTGGAGGCCTCTGGGAAGTGCTCACGGATTCTGCTCCTTGTGGCAGCTTTATGC
 AGAACCTCATCCAGGTCTAACAGAGCCTCACATGGTTCTGGAGGAGCCCCACCTCATTCAAGAGGCCCTGT
 ACGATGCCCTCCCGGAAACCATCTTCTGAAGCGACCTTACCCCTGCTCACCTTGACCCATCCTT
 AACTGCCCTCCCCCTGCTGTGCTG

Fig. 13

A**OvIL-32 alpha (SEQ ID NO:24)**

MCFARGVPHDQASLRSMHTWVDHVCDKMGNEPEEAQMEAALAEIMEEELSVDVCEWKITFKRTFPNPCR
SPVPCFRKRSKKYAAESRDPQSLPVWRTRNRKRASGPEPCGGSEVFCGVSGSGVAMY

B**OvIL-32 alpha (SEQ ID NO:25)**

CTGGGTACCGGTCCGGATTCCCGGGCAGACAGTGCAGCTGGAGCTCTGGCTGCAGGATCTCAGATC
CCAGCCGGAGGACCTAATCCACCATGTGCTTCGCTAGGGAGTCCCACATGACCAGGCTCTCTGAGGA
GCATGCTGCACACCTGGGTGGATCATGTCTGTGATAAGATGGAAATGAACCAGAAGAACAGATGGA
GGCAGCCCTAGCAGAGATGGAGGAGGAACCTCAGCAAGGATGTCTGTGAAATCATGGAAGATCACATTCAAG
AGAACCTTCCCAGTCCCTGCAGGGAGTCCAGTCCCTTGCTTCAGGAAGCGCAGCAAGAAGTACGCCGCAG
AATCCAGAGACCCCTCAGTCTCTGCCTGTCTGGAGGACAGAAACCGGAAGAGAGCATCTGGGCCAGAGCC
CTGGCGGGTTCCGAGGTTTCTGCGGAGTCTCTGGCAGCGGTGTTGCGATGTACTGACCTGGCTGCAGG
AGAAGGCAGGGCCTGCTGGAGGCCGTCTGAGTGGCTGAAGACCATCTGGGAGTGTGACGGATT
CTGCTCCTCTGTGGGGCAGCTCTCAGAAACCTCATCCAGGTCTAGGAGCCCCAGGTCGTTCTGAGGA
CTGCTCCTCATCTAGAAGGCCCTGCACAATCCCTTCCAGAAACCATCTCTGAAGCGACCTTACCC
CCTGTTCACCCCTCACCAATCCTTAACGCCCTCACCTCTGTCTGCAGGGACGACACCACAAACATCAA
GCCAGGTTCCCTCTCCAAGTCTGACCCGTCTGTCAGGGA

C**SwIL-32 alpha (SEQ ID NO:26)**

MRGVSATRTLKPAGPQPRSLGLPLPRRVPEPPPIPAESSPLLNEVRQGVRSRVRRPGHNPHYALAVR
EPRQSTFRRILELFEEMLKRLQQRWRGALAWVQERAACFRGLCRALEAFWSLVQSFCSMGHAFGSVIQ
V

D**SwIL-32 alpha (SEQ ID NO:27)**

ATGACTTGGAGGGAACTGAGCGGCCAGGCCAGCCCCCTGGAAAAGTCCTGGGTCTGTGGGCTGTTG
GCAGGAAAGCAGCCTGTGTCAGGCCAGGGCATGAGGGGGTGTCTGCCACCAGGACTCTCCCAAAGGCA
GGGCCTCAGCCAAGGTCAAGGACTGGGCTGCCCTCCCCAGGCCGGTCCCTGAACCACCCCCCATCCCTG
CAGAATCCAGTCCCTGCTCAACGAAGTCCGGCAGGGAGTCGTTCTAGAGTCCGAAGGCCTCTGGCA
CAACCCAGCCACATTATGCCCTAGGGTCCGGAGGCCAGGCAGAGCACTTCAGACGCATCCTTGAGCTG
TTGAGGAAATGCTGAAGCGCCTGCAGCAGAGGTGGAGGGGTGCCCTGGCTGGGTGAGGAAAGGGCTG
CTGCCGCTTCGGGGCTGTGCAAGGGCCCTGAGCTTCTGGAGCCTGGTGCAGAGTTTGCTCCTC
CATGGGCACGCCCTGGAGTGTCAAGGTCTAAGGTGCTCAGGTGAAATAAGAGTTCTAGAGCA
CAACCTCCCCCTGCCCTGGCTAAAAGGCAGCTGTAAGCCTT

Fig. 14